

**METHOD FOR PRODUCING BIOLOGICALLY ACTIVE HUMAN
FACTOR VIII IN THE MILK OF TRANSGENIC ANIMALS DRIVEN BY
MAMMARY-SPECIFIC EXPRESSION CASSETTES**

5

BACKGROUND OF THE INVENTION

1. Field of the invention

The present invention discloses a method for producing biologically active recombinant proteins in the milk of transgenic animals, characterized in which 10 intact human clotting factor VIII gene and B-domain deleted recombinant factor VIII gene are transferred into the mammal by gene microinjection and embryonic implantation to obtain expression and secretion in the milk of transgenic animals and their offsprings.

2. Description of the prior art

15 Hemophilia is the most common human bleeding disorder and affects approximately one in 5,000 males, causing lifelong, repeated, and potentially life-threatening hemorrhagic episodes. It results from a deficiency in functional blood coagulation factors, either in a serine protease called Factor IX (hemophilia B) or in its cofactor Factor VIII (hemophilia A). Because hemophilia is caused by 20 defects in single X-linked genes that encode circulating plasma proteins, the development of therapeutic strategies has focused on finding ways to replace the defective or deficient proteins.

Human FVIII is synthesized primarily in the liver and secreted into the circulation at low plasma concentration, approximately 100-200 ng/ml. Analysis 25 of the cloned cDNA for human FVIII (Gitschier et al., 1984, Nature 312: 326-330;

Toole et al., 1984, Nature 312: 342-347.) has provided more information about its gene and protein structure. The full length FVIII cDNA contains an open reading frame coding for a polypeptide of 2351 amino acids. This primary translation product contains a 19 a.a. signal peptides and six homologous domains in the order A1-A2-B-A3-C1-C2 (Vehar et al., 1984, Nature 312: 337-342.). The 256-kDa precursor protein is proteolytically processed intracellularly to a metal ion-linked heterodimer of a 90- to 200-kDa heavy chain (A1-A2-B) and an 80-kDa light chain (A3-C1-C2), which circulates in the plasma bound to the von Willebrand factor (vWF).

For the past two decades hemophiliacs have been treated with whole plasma, and more recently with highly purified FVIII concentrates prepared from plasma. Higher concentrates purity allows the administration of effective doses at lower volumes to patients. This therapy is effective in controlling bleeding episodes, however, hemophiliacs may suffer from other complications, compromised by the discovery that these products were transmitting human viruses such as the hepatitis B virus and human immuno-deficiency virus (HIV) to patients, many of them later developed diseases (Hoyer, 1993, Methods Enzymol. 222: 169-176).

Since then, plasma screening and viral inactivation procedures have greatly improved the safety of these products, although the potential for transmitting diseases such as Creutzfeldt-Jakob disease must be considered and has led to sporadic shortages in these plasma products. Nonetheless, when non-blood source products derived from recombinant DNA biotechnology became available, further reducing the viral risk, they were quickly embraced by caregivers and patients, despite their higher cost (Pipe and Kaufman, 2000, Nature Biotech. 18: 264-265).

One of the challenges created by the biotechnology revolution is the development of methods for the economical production of highly purified proteins in large scales. Recent developments indicate that manipulating milk composition using transgenesis has focused mainly on the mammary gland as a bioreactor to produce

5 pharmaceuticals.

SUMMARY OF THE INVENTION

The ability to modify animal genomes through microinjection technology has offered new alternatives for the manufacture of recombinant proteins.

10 Targeting the production of human recombinant protein pharmaceuticals in the milk of transgenic animals solved many problems associated with either microbial or animal cell expression systems. Bacteria often improperly fold complex proteins, introducing more involved and expensive processes. Both bacteria and yeast lack adequate post-translational modification. Bioreactors for cell cultures

15 require high capital expenditures, use large volumes of expensive culture media, and often suffer from relatively low yields.

To express a recombinant protein in the milk of a transgenic animal, expression vectors containing a gene encoding the protein of interest fused to milk specific regulatory promoter elements are generally introduced by microinjection

20 into a pronuclear-stage embryo, or alternatively transfected the expression vector into a cell line suitable for somatic cell nuclear transfer. Most of this work has been carried out with: the ovine β -lactoglobulin, rodent (mouse, rat and rabbit) whey acid protein (WAP) genes, bovine α -lactalbumin and a-s1-casein genes, as well as the caprine β -gene.

25 Several blood proteins, hormones, and enzymes have been synthesized in

transgenic animals. Of these, human FVIII is probably the largest and most complex protein to be expressed. Analysis of the cloned cDNA for human FVIII has provided more information about its gene and protein structure. The full length FVIII cDNA contains an open reading frame coding for a large polypeptide 5 of 2351 amino acids. The 256-kDa precursor hFVIII protein is proteolytically processed intracellularly to a metal ion-linked hetero-dimer of a 90- to 200-kDa heavy chain (A1-A2-B) and an 80-kDa light chain (A3-C1-C2), which circulates in the plasma bound to the von Willebrand factor (vWF). The B-domain, is encoded by a single large exon and is highly glycosylated, harboring 19 of the 25 10 N-linked glycosylation sites. The B-domain is released upon co-factor activation, so it is not necessary for clotting function.

According to the regulatory sequences employed, variable levels of expression for the recombinant human FVIII were observed. For example, using a construct containing 2.2-kb ovine β -lactoglobulin 5'-flanking sequences to drive 15 the FVIII cDNA with the introns of the murine metallothionein I (β -Lac/hFVIII-MtI), only extremely low level (4-6 ng/ml) of expression was observed in transgenic sheep (Niemann et al., 1999. Transgenic Res 8: 237-247). Whereas the hFVIII cDNA, under the control of the 2.5-kb mouse WAP promoter, was shown to secrete up to 2.7 μ g/ml in transgenic pig milk (Paleyanda et al., 1997. Nature 20 Biotech 15: 971-975).

In this invention, we describe a novel recombination of promoter, leader sequence, coding sequences and poly A tail signaling sequence as a expression cassette to generate of transgenic animals expressing the fusion gene in the mammary gland and the presence of recombinant FVIII protein ranged from 7 to 25 50 μ g/ml with over 35- to 200-fold higher than in normal human plasma, with

temporal and spatial expression profiles for clotting active rFVIII in the milk of transgenic animals in different stages of lactation.

BRIEF DESCRIPTION OF THE DRAWINGS

5

Fig.1A~1D shows a schematic map of full-length hFVIII transgene construction and detection of transgene integrated patterns in transgenic animals.

Fig.1A The structure of αLA-hFVIII-bGHpA fusion genes are shown and a pair of primer sets for PCR screening and a 1.8-kb hFVIII kpnI-fragment as probe 10 were designed flanking the 5'-end and 3'-end of hFVIII cDNA, respectively.

Fig.1B Rapid screening positive transgenic mice founders by PCR amplification. NC represented a normal mouse DNA as a negative control.

Fig.1C Screening of positive transgenic goat founders and F1 offspring by 15 PCR amplification. NC represented a normal non-transgenic goat DNA as a negative control.

Fig.1D Southern blot analysis of the integration patterns of transgene DNA in transgenic animals. Genomic DNA extracted from different founders of transgenic mice tails or transgenic goats' ear tissues were digested with BamHI and subjected to probe hybridization.

Fig.2A~2B represents the determination of hFVIII transgene copy numbers 20 in 17 transgenic founders using slot-blot hybridization.

Fig.2A The relative positions of sample loading for standard controls and transgenic founders. The standards were made with calculated hFVIII plasmid DNA, 0.5 to 20 copy numbers, mixed with 10 ug of normal mouse genomic DNA. 25 The lanes of transgenic founders were also slotted with 10 ug of undigested

genomic DNA. A kpnI fragment of hFVIII cDNA was used as a hybridization probe. Hybridization and wash was performed in high stringency condition (70°C) to avoid cross-hybridization. Result is shown in Fig.2B.

Fig.3A~3C provides a schematic map of B-domain deleted hFVIII transgene construction and detection of transgene junctional sequences.
5

Fig.3A The structure of α LA-CN-hFVIII(Δ B)-bGHpA fusion genes are shown and two pairs of primer sets for PCR screening and a 1.8-kb hFVIII kpnI-fragment as probe were designed franking the 5'-end, B-domain flanking region and 3'-end of hFVIII cDNA, respectively.

Fig.3B DNA sequencing confirmed the in-frame creation of the N-terminal α S1-casein signal peptide sequence and the 19-aa leader peptide-removed hFVIII sequence.
10

Fig.3C DNA sequencing confirmed the in-frame creation of B-domain deletion between hFVIII A-domain (A1-A2) and hFVIII C-domain (A3-C1-C2).
15

Fig.4A~4C shows the analyzed data of B domain-deleted hFVIII transgenic animals.

Fig.4A The structure of α LA-CN-hFVIII(Δ B)-bGHpA fusion genes are shown and two pairs of primer sets for PCR screening, 273-bp for the 5'-end franking region and 751-bp for the B-domain flanking region, respectively. It also shows the genomic digested enzymes and predicted patterns in Southern blot assay.
20

Fig.4B Rapid screening positive transgenic founders by PCR amplification. NC represented a normal mouse DNA as a negative control. PC represented a hFVIII(Δ B) plasmid DNA as a positive control.
25

Fig.4C Southern blot hybridization analysis of transgenic goat (Tg-3431)

harboring B-domain-deleted hFVIII fusion gene. Normal and transgenic goat genomic DNAs were digested with HindIII, PvuII, and XbaI, individually. Arrowheads represented the off-size bands in transgenic goat genome.

Fig.5 confirms the germ-line transmission of transgenic animals carrying hFVIII(Δ B) exogenic DNA in their F1 generation by using PCR detection and direct PCR product sequencing. The sequencing result exhibited the intact transgenic hFVIII(Δ B) fragment was actually present in their F1 offspring's genome.

Fig.6A~6B shows the mammary-specific expression cassette regulated a temporal and spatial expression of exogenous hFVIII RNA in transgenic animals.

Fig.6A Tissue-specific expression of α LA-FVIII transgene by RT-PCR detection. Tissue was removed from lactating mice at 7 days post partum. RNA was isolated from lactating transgenic mouse mammary gland (Ma), heart (H), liver (L), lung (Lu), muscle (M), brain (B), pancreas (P), and in male transgenic mouse mammary fat pad (F). A b-actin primer set was used as internal control.

Fig.6B Stage-specific expression of α LA-FVIII transgene during pre-partum (D-3), lactation (D1 to D22), and weaning (D29 to D36). A glyceraldehyde-3-phosphate dehydrogenase (GAPDH) primer set was used as an internal control. The ratios of hFVIII/ GAPDH band intensities were plotted by densitometer with computer analysis (Bio-Rad video densitometer, model 620).

Fig.7A~7B shows the Western blot analysis of recombinant hFVIII protein secreted from mammary glands of transgenic mice at different lactating stage.

Fig.7A The secretion of rFVIII protein in milks was collected, 10- to 20-fold diluted and subjected to western blotting with rabbit anti-hFVIII polyclonal antisera. Lane 1 contained the milk protein harvested from non-transgenic mice

5 during lactating stage as a negative control and lane 2 contained HPLC-purified hFVIII heavy chain (200-kDa) as a positive control. The orders for D7, D12, D17, and D22 represented the milk proteins harvested from various lactating stages of transgenic mice.

Fig.7B Western blotting analysis of rFVIII light chain protein with mouse anti-hFVIII monoclonal antibody D2. Lane 1 contained the milk protein harvested from non-transgenic mice during lactating stage as a negative control and lane 2 contained the HPLC-purified hFVIII light chain (80-kDa) as a positive control.

Fig.8 shows the Western blot analysis of recombinant hFVIII protein secreted from mammary glands of transgenic goat (Tg-201) at early lactating stage. The secretion of rFVIII protein in milks was collected in days 3, 11 and 22. The collected milks were diluted in 1- to 3-fold and subjected to Western blotting and hybridization with rabbit anti-hFVIII polyclonal antiserum. Lane 1 contained HPLC-purified hFVIII heavy chain (200-kDa) as a positive control and lane 2 contained the milk protein harvested from non-transgenic mice during lactating stage as a negative control.

Fig.9A~9C shows the functional assay of transgenic hFVIII protein by clotting activity analysis. The coagulant activity of hFVIII was measured by reduction of the activated partial thromboplastin time (aPTT) in a one-stage assay (Over, 1984, Scand J. Haematol. 41: 13-24.).

Fig.9A Human FVIII dilutions equivalent to a 1% to 50% dilution of normal plasma (NPP) were prepared in 50 mM imidazole buffer.

Fig.9B NPP standard curve was performed using aPTT clotting assay.

Fig.9C Control and transgenic goat milks diluted in 50%, 20%, and 10% were incubated in duplicate at 37°C in hFVIII-deficient plasma, followed by the

automated addition of aPTT reagent. The clot time, in seconds, was recorded on an ST2 Coagulometer (Stago).

BRIEF DESCRIPTION OF THE DRAWINGS

5

The invention relates to transgenic milk that can be used to produce therapeutical recombinant hFVIII for hemophilia patent treatment.

Using mammary gland-specific promoters, a wide range of proteins of biopharmaceutical interest have been expressed in rodents, pigs, and dairy animals
10 (Echeland, 1996, Current Opinion in Biotechnology 7: 536; Houdebine et al., 2000, Transgenic Research 9:505). An expression vector, comprising a gene encoding the target protein of interest fused to a milk promoter gene, is introduced by microinjection into the pronucleus of a one-cell embryo. Upon germ line integration and expression, the transgene becomes a dominant Mendelian genetic
15 characteristic that is inherited by the progeny of the founder animal. Mammalian mammary epithelial cells have the capacity to carry out complex protein synthesis with a variety of posttranslational modifications and folding. The milk of transgenic livestock presents a starting material from which human diagnostic or pharmaceutically-active and therapeutic proteins may be purified using
20 established technologies.

Milk Specific Promoters

A variety of transcriptional promoters that preferentially activate transcription in mammary epithelial cells are available. These include the promoters that control the genes encoding milk proteins such as caseins (α S1-,
25 α S2-, β -, γ -, and κ -casein), beta-lactoglobulin (Clark et al., 1989,

Bio/Technology 7: 487-492), whey acid protein (Gordon et al., 1987, Bio/Technology 5: 1183-1187), and alpha-lactalbumin (Soulier et al., 1992, FEBS Letters 297: 13). Casein promoters may be derived from the alpha, beta, gamma or kappa casein genes of any mammalian species; a preferred promoter is derived from the goat beta casein gene (DiTullio, 1992, Bio/Technology 10:74-77).

The DNA sequences of many these promoters are available, e.g., in GenBank and in scientific publications such as 1) rat alpha-lactalbumin (Richards et al., 1981, J. Biol. Chem. 256: 526-532); 2) rat WAP (Campbell et al., 1984, Nucleic Acids Res. 12: 8685-8697); 3) rat alpha-casein (Jones et al., 1985, J. Biol. Chem. 260: 7042-7050); 4) rat alpha-casein (Lee and Rosen, 1983, J. Biol. Chem. 258: 10794-10804); 5) human alpha-lactalbumin (Hall, 1987, Biochem. J. 242: 735-742); 6) bovine alpha-S1 casein (Stewart, 1984, Nucleic Acids Res. 12: 389); 7) bovine alpha-casein (Gorodetsky et al., 1988, Gene 66: 87-96); 8) bovine alpha-casein (Alexander et al., 1988, Eur. J. Biochem. 178: 395-401); 9) bovine alpha-S2 casein (Brignon et al., 1977, FEBS Letters 188: 48-55); 10) bovine alpha-lactoglobulin (Jamieson et al., 1987, Gene 61: 85-90; Alexander et al., 1989, Nucleic Acids Res. 17: 6739). For additional regulatory control or stringency, other regulatory sequences such as adjacent sequences, can be obtained from these genes or from homologous genes of other mammals using these promoter sequence as probes to screen genomic libraries.

Signal Peptide Sequences

The recombinant gene construction can also include a signal sequences, particularly a signal peptide sequences of a milk specific gene. For the best secretion efficiency of forigen protein in the mammary gland, the milk-specific signal peptide sequence can be the secretional signal sequence which naturally

occurs with the selected milk-specific promoter used in the construct, which are described below. For example, signal sequences from genes coding for caseins, e.g., alpha, beta, gamma or kappa caseins, beta lactoglobulin, whey acid protein, and lactalbumin can be used.

5 Transgenesis Constructions

A 2.0-kb promoter sequence of bovine alpha-lactalbumin (α LA) was generated by PCR amplification using a genomic DNA from high milk-producing Holstein cow, which obtained from National Taiwan University Farm, as the template. This PCR product containing entire α LA promoter and 19-aa leader sequence (SEQ ID: No. 1) or replacement with bovine α S1-casein 15-aa signal peptide sequence (SEQ ID: No.2) which created a restriction enzyme, HpaI, cloning site in the downstream sequence. These two types of promoter and signal peptide sequences were then subsequently inserted into the pCR3 vector (Invitrogen, San Diego, CA).

15 For the full-length hFVIII construction, the resulting 7.0-kb plasmid containing α LA promoter and its intact signal peptide sequence was double digested with MluI and PstI and treated with calf intestinal phosphatase (Boehringer Mannheim, Indianapolis, IN). The pCMV5/hFVIII plasmid containing the intact human FVIII coding sequence was also double digested with 20 MluI and PstI. The in frame sequence from the α LA leader peptide through the hFVIII junction was determined using the Dye Terminator sequencing system (Applied Biosystems Inc., Foster, CA). The 9.7-kb transgene consisting of 2.0-kb bovine α LA promoter, 7.2-kb hFVIII cDNA, and 0.5-kb bovine GH gene polyadenosine signal sequence was separated from plasmid pCR- α LA/hFVIII-5 25 using Clal and XbaI digestion and purified for microinjection on the twice $CsCl_2$

gradient ultra-centrifugation.

For the B domain-deleted hFVIII construction, the resulting 7.0-kb plasmid containing α LA promoter and α S1-casein signal peptide sequence was double digested with HpaI and XhoI and treated with calf intestinal phosphatase 5 (Boehringer Mannheim, Indianapolis, IN). The pCMV5/hFVIII plasmid containing the intact human FVIII coding sequence was used as template to generate a 2233-bp rhFVIII A-domain fragment using degenerate PCR, phFVIII-HpaI(+): 5'-GGT TAA CTG CCA CCA GAA GAT A-3' (SEQ ID: NO.3) and phFVIII-741aa(-): 5'-AAG CTT CTT GGT TCA ATG GC-3' (SEQ ID: NO.4), 10 and a 2085-bp rhFVIII C-domain fragment amplified by phFVIII-1643aa(+): 5'-AAG CTT GAA ACG CCA TCA ACG GGA A-3' (SEQ ID: NO.5) and phFVIII-XhoI(-): 5'-CTC GAG CCT CAG TAG AGG TCC TGT-3' (SEQ ID: NO.6), respectively. Equal molar ratio of A-domain segment, C-domain segment and pCR3- α LA vector were co-ligated and transformed into host competent cells. 15 The in frame sequence from the α S1-casein leader peptide through the hFVIII junction was determined using the Dye Terminator sequencing system (Applied Biosystems Inc., Foster, CA). The 6.8-kb transgene consisting of 2.0-kb bovine α LA promoter and aS1-casein leader sequence, 4.3-kb hFVIII cDNA, and 0.5-kb 20 bovine GH gene polyadenosine signal sequence was separated from plasmid pCR- α LA/hFVIII(Δ B) using Clal and XbaI digestion and purified for microinjection on the twice $CsCl_2$ gradient ultra-centrifugation.

Transgenic Animal Productions

The purified transgene was microinjected into the male pronuclei of fertilized eggs from superovulated female mice of the outbreed ICR strain and 25 transferred to recipient pseudo-pregnant females as previously described (Chen et

al., Transgenic Res 4: 52-59; 1995). For transgenic goat production, the pronuclear stage embryos were flushed from the donor goat's oviduct at the one and half day after insemination by means of surgical method. In order to obtain higher embryo numbers, every embryo-donating goat had been treated with 5 endocrine so as to achieve the object of superovulation. Such a superovulation treatment comprised of administrating intramuscular of follicular stimulating hormone (FSH) to the embryo-donating goat sequentially for 4 days since eighth day of estrous cycle twice a day with interval of 12 hours and the dosage was decreased daily as 4-, 3-, 2-, and 1-mg, respectively. As the first dosage at the 10 third day, co-administrated with 1000iu human chorionic gonadotropin (HCG) which resulted in detection of estrous after 54 hours whereupon gave two artificial insemination (AI) with a interval of 12 hours. Then, at about one and half days after conception, the goat one-cell stage embryos were collected with a sterile glass capillary tube via surgical embryo flushing method. The collected embryo 15 was transferred into another petri dish where it was rinsed more than ten times. Thereafter, it was placed under a phase contrast microscope at 400X amplification for gene microinjection manipulation. After a transient in vitro culture, the healthly microinjected embryos were then transferred into recipient oviducts for further conceptus development.

20 **Recombinant hFVIII Transgene Determination**

The resulting pups were rapidly screened for the transgene by PCR amplification of tail or ear tissue DNA. PCR was performed using one set of primer, p α LA-124(+): 5'-CTC TCT TGT CAT CCT CTT CC-3' (SEQ ID: NO.7) and phFVIII-149(-): 5'-GGT TAC GCG TCA AGA TTC TGA-3' (SEQ ID: NO.8), 25 which defined a 273-bp region spanning the α LA promoter, secretion signal

sequence and hFVIII cDNA junctional sequence. For the B domain-deleted hFVIII transgene detection, additional primer pairs was designed, phFVIII-ACJ(+) : 5'-AGA CTT TCG GAA CAG AGG CA-3' (SEQ ID: NO.9) and phFVIII-ACJ(-): 5'-ATC TTT TTC CAG GTC AAC ATC A-3' (SEQ ID: NO.10),
5 which defined a 751-bp region flanking A-C recombinant junction. The positive PCR screening results for transgenic animals were further confirmed by Southern blot analysis. Ten micrograms of genomic DNA were individually digested with BamHI, HindIII, PvuII, and XbaI restriction enzymes at 37 °C overnight, electrophoresed on a 0.8% agarose gel, and transferred to a Durose membrane
10 (Stratagene, La Jolla, CA). A KpnI fragment of hFVIII-specific cDNA (1.8-kb) was used as a radioactive probe to hybridize the membrane. Blots were subjected to autoradiography for three days at -20 °C.

Recombinant hFVIII RNA Expression in Transgenic Animals

The temporal and spatial expression of hFVIII RNA in transgenic animals
15 was analyzed using a reverse transcription-polymerase chain reaction (RT-PCR). Total RNA from different tissues including the heart, liver, lung, muscle, mammary gland, brain, pancreas, and kidney of female transgenic mice during lactation periods (Day 1 to Day 28 post partum) was extracted using the acid guanidinium thiocyanate method (Chomczynski and Sacchi, 1987, Anal. Biochem.
20 162: 156-159). One microgram of total RNA was treated twice with 10 units of DNase I (Gibco BRL, Gaithersburg, MD) and phenol-chloroform extracted. RNA pellets were resuspended in 15 μ l DEPC-water and then used to synthesize the first-strand cDNA with random primers and SuperScript reverse transcriptase (Gibco BRL, Gaithersburg, MD) in a total volume of 25 ml. The reaction was
25 carried out at 42 °C for 1 hr.

For further PCR amplification, an aliquot (1/10) of the RT product was adjusted to contain 0.1 μ g of each primer and additional buffer was added for a total volume of 50 μ l. PCR was performed for 30 cycles (94°C, 1 min; 55 °C, 2 min; 72°C, 2 min). The primers used included a pair of hFVIII-specific primers,
5 phFVIII-F2(+):5'-CAT TCT ATT CAT TTC AGT GGA CA-3' (SEQ ID: NO.11) and phFVIII-R2(-): 5'-GAG ATG TAG AGG CTG GAG AAC T-3' (SEQ ID: NO.12), and a pair of glyceraldehydes-3-phosphate dehydrogenase (GAPDH), as well as a pair of β -actin. Both β -actin and GAPDH are the universal transcripts in every cell and were used as the internal controls of RT-PCR.

10 **Immunoblot Analysis of Transgenic Milk Proteins**

Milk was collected from lactating females as previously described (Simons et al., 1987, Nature 328: 530-532.) and analyzed using SDS-polyacrylamide gel electrophoresis (SDS-PAGE) (Cheng et al., 1998, Human Gene Therapy 9: 1995-2003). Ten- to twenty-fold dilutions of the collected milk, in 75 mM Tris-HCl
15 buffer at pH 6.8, from different lactation periods were diluted in SDS-PAGE sample buffer with 5% 2-mercaptoethanol and electrophoresed on 7.5% gel. To estimate production levels, HPLC-purified recombinant hFVIII standard was diluted to 10 μ g/ml in normal mouse milk and electrophoresed alongside the transgenic milk samples. Proteins were electrotransferred from the gel to a PVDF membrane (NEN Life Science Products, Boston, MA). The blots were probed with primary antibodies recognizing hFVIII at 2 to 10 μ g/ml and washed with phosphate-buffered saline containing 0.1% Tween-20 (PBS-T). Blots were reacted with horseradish peroxidase (HRP)-conjugated second antibodies at 0.2 mg/ml.
20 Polyclone antibody C6 recognize the heavy chain of hFVIII rang from 80-200 kDa and monoclonal antibody D2 recognize the light chain of hFVIII at 75-80 kDa.
25

The blot was then developed with the chemiluminescent ECLTM detection system (Amersham, UK) and exposure to x-ray film. Band intensities were compared by densitometry.

Secretion of hFVIII protein from the transgenic milk was determined quantitatively with the enzyme-linked immunosorbent assay (ELISA) as previously described (Chen et al., 1993, J Virol 67: 2142-2148). Briefly, plates were coated with capture antibodies (ESH-5 and ESH-8, 500ng each per well; American Diagnostics, Greenwich, CT) in carbonate buffer and incubated for 1 hour at 37 °C. Plates were washed with 0.05% Tween-20 in phosphate-buffered saline (PBS) and blocked in 50 mM Tris (pH 7.2), 150 mM NaCl, 0.5% gelatin, and 0.05% Tween-20 for 2 hour at 37 °C. Purified recombinant FVIII (Hyland, Baxter Healthcare, CA), prepared in blocking buffer with 1:50 normal murine milk, served as the standard. Samples and standards were incubated for 1 hour at 37°C. Detection antibody (rabbit anti-human FVIII 1: 10,000 dilution) was added and allowed to react with hFVIII at 37°C for 1 h. After removing the first antibody using four washes with PBS, a second antibody, goat anti-rabbit immunoglobulin antibody conjugated with horseradish peroxidase, was added (1: 3,000 dilution) for a further 1 h of incubation. The plates were washed again thoroughly with PBS, and 100 μ l of substrate solution (2 mg of o-phenylenediamine dissolve in 1 ml of 1M phosphate citrate plus 0.02% H_2O_2) was added for development. After 30 min, 100 μ l of 1M H_2SO_4 was added immediately to stop the reaction and the colors were measured by optical density at 492 nm.

The Feature of α -Lactalbuimn Mammary Expression Cassette

25 Expression of rFVIII protein in the milk of transgenic animals driven by

bovine α -lactalbuimn regulatory sequence seems more efficient than the other transgene constructions, which were controlled by ovine β -lactoglobulin promoter (Niemann et al., 1999, Transgenic Res 8: 237-247.) as well as mouse WAP regulatory sequence (Paleyanda et al., 1997, Nature Biotech 15: 971-975).

5 Expression of the bovine α LA gene has been shown to be the most lactation-specific of all bovine milk protein genes (Goodman and Schanbacher, 1991, Biochem Biophys Res Commun 180:75-84). Use of the α LA 19-aa secretary peptide (SEQ ID: NO: 13) or α S1-casein 15-aa signal peptide (SEQ ID: NO: 14) to lead the rFVIII protein secretion and the bGH polyadenylation signal to 10 stabilize the steady-state of hFVIII RNA molecules, which may also have contributed to our success. Actually, there are several previous reports demonstrated that mammary specific transgenes driven by α LA promoter have resulted in high levels of gene expression up to 3.7 mg/ml (Hochi et al., 1992, Mol Reprod Dev 33: 160-164; Soulier et al., 1992, Fed Eur Biol Soc Lett 297: 13- 15 20; Maschio et al., 1991, Biochem J 275:459-465) in their milks. This characteristic of the bovine α LA gene makes its regulatory elements potentially useful as a mammary expression system in transgenic animals. In contrast to the caseins and b-lactoglobulin, the production of α LA mRNA increases suddenly at 20 25 parturition, remains elevated during lactation, and drops sharply at dry-off and during involution. The rFVIII protein profile lead by the α LA promoter and 19-aa secretion signal peptide or α S1-casein 15-aa signal peptide follows a similar trend. The lactation specificity of the regulatory regions used to control mammary expression in transgenic animals may be important when foreign proteins that have biological activities are expressed because these proteins may exhibit their biological function in the animals if they are secreted before tight junctions of

mammary epithelial cells are formed.

The Feature of hFVIII Protein Expression

Clotting factor IX (FIX), adenosine deaminase (ADA), and other cDNAs were expressed at high levels from retroviral vectors in rat fibroblasts (Miller,
5 1992, Nature 357: 455-460; Palmer et al., 1991, Proc Natl Acad Sci USA 88: 1330-13334), whereas the FVIII cDNA was expressed at very low levels from these vectors in primary human fibroblast cells (Hoeben et al., 1990, J Biol Chem 265: 7318-7323; Lynch et al., 1993, Hum Gene Ther 4: 259-272). It has been found that FVIII RNA steady-state levels were reduced 100-fold from a FVIII
10 retroviral vector compared to the same vector expressing other cDNAs, and FVIII vector titers were correspondingly reduced 100-fold compared to other vectors (Lynch et -al., 1993, Hum Gene Ther 4: 259-272). A large part of the inhibitory effect of the FVIII cDNA on expression from a retroviral vector has been localized to a 1.2-kb fragment, derived from the A2 and A3 domains, which
15 decreased the steady-state RNA levels 100- to 200-fold and decreased vector titers 10-fold (Koeberl et al., 1995, Hum Gene Ther 6: 469-479). The mechanism by which the FVIII cDNA inhibitory sequence (INS) decreases RNA and protein expression from expression vectors remain to be established. Recently, experimental data provided ample evidence that the human FVIII cDNA contains
20 elements that repress its own expression at the level of transcription (Hoeben et al., 1995, Blood 85: 2447-2454). Fallaux and coworkers (1996, Mol Cell Biol 16: 4264-4272) identified a 305-bp region derived from exons 9 to 11 that encodes a nuclear-matrix attachment region (MAR), also called the scaffold-attached region (SAR). Yeast MARs elements can play an important role in transcriptional
25 silencing (Newlon and Theis, 1993, Transgenic Res 8: 237-247). The B domain

can be deleted without any significant effect on specific procoagulant activity (Pittman et al., 1993, Blood 81:2925-2935; Chao et al., 2000, Blood, 95: 1594-1599). B-domain-deleted hFVIII cDNA (BDD-hFVIII) is 4.3 kb and primary truncate polypeptide (hFVIII \triangle B) is 1448 aa (SEQ ID: NO.15) not thought
5 feasible for testing in transgenic animals previously.

The present invention is further depicted in the illustration of examples, but the descriptions made in the examples should not be construed as a limitation on the actual application of the present invention.

10

EXAMPLE 1

Generations of transgenic mice, pigs and goats carrying the full-length hFVIII gene in mammary-specific expression cassette

Out of 79 potential transgenic founder mice, 17 were identified as being transgenic by the PCR screening (Fig. 1B). Two transgenic founder goats carrying
15 the full-length hFIII also have been identified by PCR screening (Fig. 1C) as well as two lines of transgenic pigs have been established. To quantify the transgene copy numbers and to understand the integration patterns of the foreign gene within the genome the transgenic animals, restriction enzyme BamHI was used to digest the genomic DNA, cut once within the transgene, and subjected to Southern blotting analysis. On hybridization using the 1.8-kb KpnI fragment of human-specific FVIII sequence as a probe (Fig. 1A), a 9.7-kb band representing monomeric transgene copies present in head-to-tail joining (H-T) tandem repeats was observed in all cases. A 4.6-kb hybridization band was observed in the blots of all transgenic mice present in tail-to-tail joining (T-T) inverted repeats (Fig.
20 1D). Different intensities of the hybridization signal were also observed indicating
25

the presence of different transgene copy numbers in these mice. Further detail quantification using slot-blot hybridization (Fig. 2A~2B), they could be distinguished into three groups according to the copies of transgene integration. For low copy number (defined as 1-5 copies per cell), there were six transgenic 5 lines including α LAF-7, -15, -33, -36, -43 and -54. Transgenic founders carrying middle copy number (10-20 copies per cell) were found in nine lines including α LAF-9, -13, -18, -27, -28, -29, -30, -38 and -39. In addition, there were two lines (α LAF-8 and -25) carrying high copy number (40-50 copies per cell) of hFVIII transgene in their genome. All of the transgenic mice harboring α LA-hFVIII 10 DNAs presented two-to-three off-size bands (Fig. 1D) besides the predicted transgene junctions. These bands were probably rearranged transgene sequences, some of which were integration sites representing transgene-cellular junctions.

Breeding lines were established from all transgenic founder animals by crossing them with normal ICR mice, Alpine goats (Fig. 1C), or hybride pigs. The 15 multiple integrated copies of the transgene were found to be stably germ-line transmitted among twelve (7 females and 5 males) out of the 17 transgenic founders.

EXAMPLE 2

20 **Generations of transgenic mice and goats carrying the B-domain deleted hFVIII gene in mammary-specific expression cassette**

B-domain deleted hFVIII transgene construct driven by α LA promoter and α S1-casein secretary peptide sequence was shown in Fig. 3A. In N-terminal of rhFVIII polypeptide, a 15-aa α S1-casein signal peptide was added for leading 25 newly synthesized rhFVIII secretion into mammary ductal cavity (Fig. 3B). In the

middle of rFVIII polypeptide, the A-domain (741-residue) has been created to join the C-domain (1643-residue) for completely deleted the B-domain segment (Fig. 3C).

Out of 65 potential transgenic founder mice, 15 were identified as being
5 transgenic by the two sets of primers, one pair of primer located in 5'-promoter junction, the other pair of primer flanking the B-domain deletion region (Fig. 4A). The PCR screening was shown in Fig. 4B. To quantify the transgene copy numbers and to understand the integration patterns of the foreign gene within the genome of the transgenic mice, restriction enzyme HindIII, PvuII, and XbaI were
10 used to digest the genomic DNA, cut once within the transgene, and subjected to Southern blotting analysis (Fig. 4C). The result showed that transgenic goat (Tg-3431) harboring B-domain-deleted hFVIII fusion gene clearly exhibited one to two off-size bands in their genome when comparing with normal goat genome.

Germ-line transmission ability of transgenic animals carrying hFVIII(Δ B)
15 exogenic DNA in their F1 generation was confirmed by using PCR detection and direct PCR product sequencing. The sequencing result exhibited the transgenic hFVIII(Δ B) fragment was actually present in their F1 offspring's genome of transgenic goats (Fig. 5).

20

EXAMPLE 3

Temporal and spatial expression of exogenous hFVIII RNA in transgenic animals driven by mammary-specific expression cassette

To characterize the spatial expression of the new developed mammary-specific expression cassette containing hFVIII in this invention, total tissue RNAs
25 were extracted from different organs in the breeding lines established from the

transgenic founder mice. Reverse-transcriptional polymerase chain reaction (RT-PCR) analysis was performed using two pair of primer sets, one was phFVIII-F2(+) (SEQ ID: NO.11) and phFVIII-R2(-) (SEQ ID: NO.12) specific to human FVIII cDNA franking 3'-coding region, the other was b-actin primer set as an internal control. As shown in Fig. 6A, the transgene expressed transcriptant of the 410-bp hFVIII RT-PCR product was found in the mammary gland of lactating transgenic mouse. No homologous transcripts were detectable in the heart (H), liver (L), lung (LU), muscle (M), brain (B), prancreas (P), or in male transgenic mouse mammary fat pads (F). All examined tissues showed a 420-bp amplified fragment for mouse b-actin to assess the integrity and quantity of RNA in each sample. The efficiency of DNase I treatment to eliminate DNA contamination was determined using RNA from a transgenic mammary gland. When the reverse transcriptase was omitted from the reaction, no amplification was observed (Fig. 6A, last lane).

Temporal expression studies were performed on the F1 transgenic mice in the breeding lines established from founder mice α LAF-15 and -18. Total RNAs were extracted at different physiological states in the transgenic mammary gland using tissue biopsies subjected to RT-PCR detection. The results showed that the recombinant hFVIII mRNA was expressed in all lactating periods (D1, D8, D15 and D22, shown in Fig. 6B), whereas the same transcripts were not detectable in the later stages of pregnancy before parturition (D-3) and in the weaning stage after lactation (D29 and D36, in Fig. 6B). The 2.0-kb bovine α LA promoter had a highly tissue-specific and stage-specific gene regulation activity in the mammary epithelial cells during the lactation period.

To quantify the level of hFVIII mRNA in the mammary glands of

transgenic mice, densitometric analysis was performed, comparing the intensity of the 250-bp band in each lane normalized to the level of signal generated upon co-amplification of the mouse glyceraldehyde-3-phosphate dehydrogenase (GAPDH) primers. The intensity of the hFVIII transcript increased eight-fold and ten-fold 5 upon Day 8 and Day 15 post-parturition, respectively, while a two-fold decrease was present on Day 22 of the later lactation (Fig. 6B), compared to Day 1 of the newly lactating stage.

EXAMPLE 4

10 **Expression and secretion of recombinant hFVIII proteins into the transgenic milks**

To determine the production of recombinant hFVIII and to compare the secretion efficiency of rFVIII among the different transgenic mouse lines, milk was collected from five lines of F0, F1 and F2 females during lactation. Proteins 15 from both non-transgenic control and transgenic skim milks were separated in SDS-PAGE and followed by Western blot analysis (Fig. 7A~7B). No polypeptides characteristic of recombinant hFVIII were detected in control mouse milk using the hFVIII-specific polyclonal antibody. In transgenic milk, rFVIII was detected as a heterogenous group of polypeptides of approximately 80-200 20 kDa, of which the 92-200 kDa polypeptides represent the heavy chain and its proteolytic cleavage products or different glycosylational modification patterns. The small molecule of an 80 kDa corresponding to the light chain containing hFVIII C2 domain was also detected by this antibody (Fig. 7A). In similar experiments using monoclonal antibodies that recognize specific hFVIII light 25 chain C2 domain structures, a specific polypeptide corresponding in size to the 80

kDa was observed as compared with the HPLC-purified hFVIII C2 domain peptide (Fig. 7B).

In the transgenic goat (Tg-201), milk was collected from days 3, 11 and 22 during early lactation stage for Western blot assay (Fig. 8). No polypeptides 5 characteristic of recombinant hFVIII were detected in control goat milk using the hFVIII-specific polyclonal antibody. In transgenic milk, rFVIII was detected as a heterogenous group of polypeptides of approximately 80-200 kDa, which represent the heavy chain and its proteolytic cleavage products or different glycosylation modification patterns.

10

EXAMPLE 5

Biological function assay for clotting activity of recombinant hFVIII derived from transgenic milks

The coagulant activity of hFVIII was measured by reduction of the 15 activated partial thromboplastin time (APTT) in a one-stage assay (Over, 1984, Scand J. Haematol. 41: 13-24.). Human FVIII dilutions equivalent to a 1:10 to 1:120 dilution of normal plasma were prepared in 50 mM imidazole buffer, pH 7.4, containing 100mM sodium chloride, 0.1% BSA and 0.01% Tween-20. Control and transgenic mouse milks diluted 1:20, 1:30, and 1:40 were incubated in 20 duplicate at 37 °C in hFVIII-deficient plasma (Sigma Diagnostics, St. Louis, MO), followed by the automated addition of APTT reagent (Dade Behring, Marburg, Germany). Clot formation was initiated by the addition of 35 mM $CaCl_2$. The clot time, in seconds, was recorded on an ST2 Coagulometer (Stago). Semi-logarithmic analysis was used to plot the clot time versus amount of FVIII. 25 Control mouse milk gave results similar to the reagent blank.

The concentrations of rFVIII ranged from 7.0 to 50.2 μ g/ml, over 35- to 200-fold higher than that in normal human plasma (Table 1). The expression levels of rFVIII from three groups on different line carrying low, middle and high copy numbers of transgenes were not significantly different. Recombinant hFVIII production generally tended to increase through the lactation period, but dropped dramatically at the end of lactation. This result was in parallel with the RNA transcript assay (Fig. 6A~6B) as well as the typical mouse milk production curve, mouse milk yield increased throughout lactation, peaked approximately D15 of lactation, and then decreased dramatically after D20.

The functional activity of rFVIII was examined using one-stage clotting assays (Table 1) and this approach demonstrated that rFVIII secreted in the milk of transgenic mice was biologically active. In the clotting assay, the addition of transgenic mouse milk, but not control milk, to FVIII-deficient human plasma resulted in the restoration of normal coagulant activity. Up to 13.41 U/ml of rFVIII procoagulant activity was detected. The activity of rFVIII was detected throughout lactation as shown in Table 1. The same result for rFVIII clotting activity derived from transgenic goat also has been demonstrated and showed in Fig. 9A~9C.

Table 1. Recombinant hFVIII concentration and coagulation activity in the milk of transgenic animals with different groups of transgene copy, lines and generations

No. of transgenic rFVIII concentration	Lactations and days (L/D)	Coagulation activity assay (U/ml) ^a	(μg/ml)
Low copy group(1-5 copies)			
aLAF15 (F0) (n=1)	L1/D7 L1/D12 L1/D19	4.82 ± 0.43 7.11 ± 0.76 3.60 ± 0.51	22.84 ± 1.65 30.58 ± 1.37 19.87 ± 0.96
aLAF36 (F1) (n=4)	L1/D7 L1/D17 L2/D7 L2/D17	6.38 ± 1.85 5.64 ± 2.66 13.41 ± 2.87 9.46 ± 2.04	29.26 ± 3.58 24.92 ± 3.04 50.21 ± 5.73 40.84 ± 4.91
Middle copy group(10-20 copies)			
aLAF18 (F1) (n=3)	L1/D7 L1/D12 L1/D17	0.98 ± 0.39 6.14 ± 0.98 8.91 ± 2.15	7.03 ± 2.56 32.07 ± 4.30 41.37 ± 7.78
aLAF28 (F2) (n=3)	L1/D7 L1/D12 L2/D17	3.01 ± 0.95 6.55 ± 2.07 7.81 ± 2.53	9.23 ± 3.74 35.56 ± 6.08 38.11 ± 5.72
High copy group(40-50copies)			
aLAF25 (F1) (n=3)	L1/D8 L1/D15 L1/D21	11.28 ± 2.33 8.72 ± 1.79 1.56 ± 0.24	46.33 ± 4.57 32.92 ± 3.97 15.08 ± 4.84
aLAF25 (F2) (n=3)	L1/D8 L1/D15 L1/D21	7.92 ± 2.01 8.58 ± 2.78 1.22 ± 0.61	39.29 ± 6.89 43.48 ± 5.21 13.32 ± 5.05

^a One unit of rFVIII was defined as equivalent to the amount of human FVIII normally present in 1ml of plasma, approximately 200 ng. Results presented are the average of two independent assays

THE ADVANTAGES OF THE INVENTION

1. The new developed mammary-specific expression cassette containing three important parts:
 - (1) 2.0-kb bovine α LA gene promoter which has been shown to be the most lactation-specific of all bovine milk protein genes;
 - (2) use of the α S1-CN 15-aa or α LA 19-aa as a secretary peptide to lead the rFVIII protein secretion; and
 - (3) the bGH polyadenylation signal to stabilize the steady-state of hFVIII RNA molecules, which can guaranty the highly expression and efficiently secretion of any exogenic proteins.
2. Transgenic expression delivers the advantages of mammalian cells such as a sophisticated refolding machinery and glycosylation.
3. Transgenic productions are scale-up flexibility since the herd size can be increased rapidly and inexpensively, as well as the relative low-cost and low complexity of the raw product manufacturing facilities as compared to more traditional cell culture facilities.
4. Biological active recombinant hFVIII protein derived from transgenic milks is easily collected by diary automatic milk collection system and simply purified procedure to obtain the massive recombinant proteins.
- 20 5. Transgenic mice, goats and pigs expressing high levels of rFVIII either in full-length gene constructs or in B domain-deleted hFVIII will be a great value system for the mass production of biologically active rFVIII in transgenic farm animals.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

 (iii) NUMBER OF SEQUENCES: 15

5. (2) INFORMATION FOR SEQ ID NO: 1:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 63 nucleotides

 (B) TYPE: nucleic acid

 (C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: artificial synthetic DNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGATGTCCT TTGTCTCTCT GCTCCTGGTA GGCATCCTAT TCCATGCCAC

CCAGGCTGTT AAC 63

15

(2) INFORMATION FOR SEQ ID NO: 2:

 (i) SEQUENCE CHARACTERISTICS:

 (A) LENGTH: 50 nucleotides

 (B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: artificial synthetic DNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGAAACTTC TCATCCTTAC CTGTCTTGTG GCTGTTGCTG CCAGGTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 22 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGTTAACTGC CACCAGAAGA TA 22

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGCTTCTTG GTTCAATGGC 20

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

5 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AAGCTTGAAA CGCCATCAAC GGGAA 25

10 (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CTCGAGCCTC AGTAGAGGTC CTGT 24

20 (2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

5 CTCTCTTGTGTC ATCCTCTTCC 20

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 nucleotides

10 (E) TYPE: nucleic acid

(F) STRANDEDNESS: single

(G) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

15 GGTTACGGGT CAAGATTCTG A 21

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 nucleotides

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

AGACTTTCGG AACAGAGGCA 20

(2) INFORMATION FOR SEQ ID NO: 10:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATCTTTTCC AGGTCAACAT CA 22

(2) INFORMATION FOR SEQ ID NO: 11:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 nucleotides

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTCTATTC ATTCAGTGG ACA 23

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 nucleotides

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GAGATGTAGA GGCTGGAGAA CT 22

10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: Amino acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

20 Met Met Ser Phe Val Ser Leu Leu Leu Val Gly Ile Leu Phe His

1 5 10 15

Ala Thr Glu Ala

(3) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(E) LENGTH: 15 amino acids

(F) TYPE: Amino acid

5 (G) STRANDEDNESS: single

(H) TOPOLOGY: linear

(ii) MOLCULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Lys Leu Leu Ile Leu Thr Cys Leu Val Ala Val Ala Ala Arg
10 1 5 10 15

(3) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(I) LENGTH: 1448 amino acids

15 (J) TYPE: Amino acid

(K) STRANDEDNESS: single

(L) TOPOLOGY: linear

(ii) MOLCULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

20 Met Lys Leu Leu Ile Leu Thr Cys Leu Val Ala Val Ala Ala Arg
1 5 10 15
Leu Thr Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
20 25 30

	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala
							35			40				45	
	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser
							50			55				60	
5	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu
							65			70				75	
	Phe	Asn	Ile	Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly
							80			85				90	
	Pro	Thr	Ile	Gln	Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu
10						95				100				105	
	Lys	Asn	Met	Ala	Ser	His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val
							110			115				120	
	Ser	Tyr	Trp	Lys	Ala	Ser	Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr
							125			130				135	
15	Ser	Gln	Arg	Glu	Lys	Glu	Asp	Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser
							140			145				150	
	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	Lys	Glu	Asn	Gly	Pro	Met	Ala
							155			160				165	
	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	Tyr	Leu	Ser	His	Val	Asp
20							170			175				180	
	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	Gly	Ala	Leu	Leu	Val
							185			190				195	

	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	Gln	Thr	Leu	His
					200					205					210
	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	Lys	Ser	Trp
					215					220					225
5	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	Ala	Ala
					230					235					240
	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	Val
					245					250					255
	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val
10					260					265					270
	Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser
					275					280					285
	Ile	Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln
					290					295					300
15	Ala	Ser	Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr
					305					310					315
	Leu	Leu	Met	Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser
					320					325					330
	Ser	His	Gln	His	Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser
20					335					340					345
	Cys	Pro	Glu	Glu	Pro	Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala
					350					355					360

	Phe	Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	
																530
																535
	Ser	Asp	Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	
																545
																550
5	Met	Glu	Arg	Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	
																560
																565
	Cys	Tyr	Lys	Glu	Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	
																575
																580
	Asp	Lys	Arg	Asn	Val	Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	
10																590
																595
	Ser	Trp	Tyr	Leu	Thr	Glu	Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	
																605
																610
	Ala	Gly	Val	Gln	Leu	Glu	Asp	Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	
																620
																625
15	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	Phe	Asp	Ser	Leu	Gln	Leu	Ser	
																635
																640
	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	Tyr	Ile	Leu	Ser	Ile	Gly	
																650
																655
	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	Ser	Gly	Tyr	Thr	Phe	
20																665
																670
	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	Leu	Phe	Pro	Phe	
																680
																685
																690

	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro	Gly	Leu	Trp
					695					700					705
	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	Met	Thr
						710				715					720
5	Ala	Leu	Leu	Lys	Val	Ser	Ser	Cys	Asp	Lys	Asn	Thr	Gly	Asp	Tyr
					725					730					735
	Tyr	Glu	Asp	Ser	Tyr	Glu	Asp	Ile	Ser	Ala	Tyr	Leu	Leu	Ser	Lys
					740					745					750
	Asn	Asn	Ala	Ile	Glu	Pro	Arg	Ser	Leu	Lys	Arg	His	Gln	Arg	Glu
10					755					760					765
	Ile	Thr	Arg	Thr	Thr	Leu	Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr
					770					775					780
	Asp	Asp	Thr	Ile	Ser	Val	Glu	Met	Lys	Lys	Glu	Asp	Phe	Asp	Ile
					785					790					795
15	Tyr	Asp	Glu	Asp	Glu	Asn	Gln	Ser	Pro	Arg	Ser	Phe	Gln	Lys	Lys
					800					805					810
	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr
					815					820					825
	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	Asn	Arg	Ala	Gln	Ser
20					830					835					840
	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	Gln	Glu	Phe	Thr
					845					850					855

	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	Leu	Asn	Glu	
																860
																865
																870
	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	Glu	Asp	
																875
																880
																885
5	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Ser	
																890
																895
																900
	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	
																905
																910
																915
	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	
10																920
																925
																930
	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	
																935
																940
																945
	Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	
																950
																955
																960
15	Lys	Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	
																965
																970
																975
	Thr	Asn	Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	
																980
																985
																990
	Glu	Phe	Ala	Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	
20																995
																1000
	Tyr	Phe	Thr	Glu	Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	
																1010
																1015
																1020

	Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	
																1190
																1195
																1200
	Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	
																1205
																1210
																1215
5	Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	
																1220
																1225
																1230
	Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	
																1235
																1240
																1245
	Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	
10																1250
																1255
																1260
	Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	
																1265
																1270
																1275
	Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys	
																1280
																1285
																1290
15	Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln	
																1295
																1300
																1305
	Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser	
																1310
																1315
																1320
	Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp	
20																1325
																1330
	Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe	
																1340
																1345
																1350

Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys
1355 1360 1365

Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser
1370 1375 1380

5 Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys
1385 1390 1395

Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val
1400 1405 1410

Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His
1415 1420 1425

10 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu
1430 1435 1440

Gly Cys Glu Ala Gln Asp Leu Tyr
1445